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01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79																					

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XX 158. 11-01-2012 (first entry)
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XX 171. 24-02-2013 (first entry)
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XX 172. 25-03-2013 (first entry)
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XX 173. 26-04-2013 (first entry)
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XX 174. 27-05-2013 (first entry)
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XX 175. 28-06-2013 (first entry)
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XX 176. 29-07-2013 (first entry)
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XX 177. 30-08-2013 (first entry)
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XX 178. 31-09-2013 (first entry)
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XX 179. 01-10-2013 (first entry)
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XX 180. 02-11-2013 (first entry)
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XX 181. 03-12-2013 (first entry)
XX
XX 182. 04-01-2014 (first entry)
XX
XX 183. 05-02-2014 (first entry)

[illegible]

neuropathic pain, nociceptive pain, the disorder is inflammation or a cardiovascular disease. A cardiac rhythm of the heart is not a pain alleviating pain in a mammal in pain or about to be subjected to a pain inducing event, and to treat disorders associated with radical depolarisation of excitable membranes by a treatment a KATP channel. The disorders include cardiac, vascular and cerebral ischaemia and asthma.

Sequence: 4 AA:

Query Match: 84.6% Score: 127.0E 22 Length: 41
 Best Local Similarity: 84.6% Prod. No.: 9,4e-08
 Matches: 22 Conservative: 0 Mismatches: 4 Indels: 0 Gaps: 0
 2 CXXXXXPSHHGGYSGKAVPT 27
 1 | 11111 111 111 111111
 1b 6 CXXXXXPSHHGGYSGKAVPT 41

FIGURE 12

AM06041

AM06041 standard: peptide: 41 AA

AM06041

24-oct-2001 (first entry)

24-oct-2001 (first entry)

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neuropathic pain, nociceptive pain, the disorder is inflammation or a cardiovascular disease. A cardiac rhythm of the heart is not a pain alleviating pain in a mammal in pain or about to be subjected to a pain inducing event, and to treat disorders associated with radical depolarisation of excitable membranes by a treatment a KATP channel. The disorders include cardiac, vascular and cerebral ischaemia and asthma.

Sequence: 4 AA:

Query Match: 84.6% Score: 127.0E 22 Length: 41
 Best Local Similarity: 84.6% Prod. No.: 9,4e-08
 Matches: 22 Conservative: 0 Mismatches: 4 Indels: 0 Gaps: 0
 2 CXXXXXPSHHGGYSGKAVPT 27
 1 | 11111 111 111 111111
 1b 6 CXXXXXPSHHGGYSGKAVPT 41

FIGURE 13

AM06041

AM06041 standard: peptide: 41 AA

AM06041

24-oct-2001 (first entry)

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[illegible]

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[illegible]

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 2 ANTI-SENSE: No
 3 ORIGINAL SOURCE:
 4 ORGANISM: Atax robustus
 5 FEATURE:
 6 NAME/KEY: Modified-site
 7 LOCATION: 37
 8 OTHER INFORMATION: /label-a
 9 OTHER INFORMATION: "this site may be antibody without loss
 10 OTHER INFORMATION: of biological activity"
 11 US-08-687489A-4

Query Match: 40.1%; Score 61; ID: 47;
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 4 11 1 11 1 1
 2 11 1 11 1 1
 4 11 1 11 1 1

RESULT 2

1 US-08-687489A-4
 2 Sequence 4; Application US/0864314
 3 Patent No. 6959182

GENERAL INFORMATION:

1 APPLICANT: ALKERMES, INC.
 2 APPLICANT: HOFFER, MARCEL E.H.
 3 APPLICANT: TYLER, MARGARET E.
 4 APPLICANT: WONG, EDWARD J.

1 TITLE OF INVENTION: Insecticidal Toxins derived from
 2 NUMBER OF INVENTION: 1; Filed with a view of having an effect on

1 ADDRESS: 25
 2 ADDRESS: 25

1 ADDRESS: 25
 2 ADDRESS: 25

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1 ANTI-SENSE: No
 2 ORIGINAL SOURCE:
 3 ORGANISM: Atax robustus
 4 FEATURE:
 5 NAME/KEY: Modified-site
 6 LOCATION: 37
 7 OTHER INFORMATION: /label-a
 8 OTHER INFORMATION: "this site may be antibody without loss
 9 OTHER INFORMATION: of biological activity"
 10 US-08-687489A-4

Query Match: 40.1%; Score 61; ID: 47;
 Post Local Similarity: 47.8%; Prod. No. 0.82;
 Matches: 11; Conservation: 4; Mismatches: 7; Indels: 2; Gaps: 1;
 2 11 1 11 1 1
 4 11 1 11 1 1
 2 11 1 11 1 1
 4 11 1 11 1 1

RESULT 3

1 US-08-687489A-4
 2 Sequence 6; Application US/0864314
 3 Patent No. 6955573

GENERAL INFORMATION:

1 APPLICANT: ALKERMES, INC.
 2 APPLICANT: HOFFER, MARCEL E.H.
 3 APPLICANT: TYLER, MARGARET E.
 4 APPLICANT: WONG, EDWARD J.

1 TITLE OF INVENTION: Insecticidal Toxins derived from
 2 NUMBER OF INVENTION: 1; Filed with a view of having an effect on

1 ADDRESS: 25
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Patent No. 576,554

INVENTOR: ROBERT N. ...

ATTORNEY: ...

ADDRESS: ...

CITY: ...

STATE: ...

COUNTRY: ...

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: ...

FILING DATE: ...

APPLICATION DATE: ...

ATTORNEY/AGENT INFORMATION:

NAME: ...

REGISTRATION NUMBER: ...

TELEPHONE: ...

TELEFAX: ...

INFORMATION: ...

LENGTH: ...

TYPE: ...

MOLECULE TYPE: ...

HYPOTHETICAL: ...

ANTI-SENSE: ...

ORGANISM: ...

FEATURES:

NAME/KEY: ...

LOCATION: ...

OTHER INFORMATION: ...

OTHER INFORMATION: ...

OTHER INFORMATION: ...

US-09-749-637a-271

Query Match: 32.98; Score 50; DB 1; Length 47;

Best Local Similarity: 43.53; Prod. No. 14;

Matches: 10; Conserved: 3; Mismatches: 8; Indels: 2; Gaps: 1;

QY 2 C1XSDCEHSDHDSKCAP 24

11 1 1 1 1 1

DB 4 C1XSDCEHSDHDSKCAP 24

RESULT: 10

US-09-749-637a-271

Sequence 8: Application US/09/749-637a-271

Patent No. 595,018

GENERAL INFORMATION:

ATTORNEY: ...

ADDRESS: ...

CITY: ...

STATE: ...

COUNTRY: ...

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: ...

FILING DATE: ...

APPLICATION DATE: ...

ATTORNEY/AGENT INFORMATION:

NAME: ...

REGISTRATION NUMBER: ...

TELEPHONE: ...

TELEFAX: ...

INFORMATION: ...

LENGTH: ...

TYPE: ...

MOLECULE TYPE: ...

HYPOTHETICAL: ...

ANTI-SENSE: ...

ORGANISM: ...

FEATURES:

NAME/KEY: ...

LOCATION: ...

OTHER INFORMATION: ...

OTHER INFORMATION: ...

OTHER INFORMATION: ...

US-09-749-637a-271

Query Match: 32.98; Score 50; DB 1; Length 47;

Best Local Similarity: 43.53; Prod. No. 14;

Matches: 10; Conserved: 3; Mismatches: 8; Indels: 2; Gaps: 1;

QY 2 C1XSDCEHSDHDSKCAP 24

11 1 1 1 1 1

DB 4 C1XSDCEHSDHDSKCAP 24

RESULT: 11

US-09-749-637a-271

Sequence 5: Application US/09/749-637a-271

Patent No. 595,018

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HYPERTEXT: No
 ANTI SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Atax robustus
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 47
 OTHER INFORMATION: /label 4
 OTHER INFORMATION: /note "this site may be amplified without loss
 of information of biological activity"
 US 08 943 414 4

Query Match 49.5% Score 709 Lb 17 Length 47
 Best Local Similarity 52.2% Prod. No. 0.054
 Matches 125 Conservative 43 Mismatches 62 Indels 27 Gaps 13

UY 4 CIPSDCPSDHCOSGKAF 26
 1111 1 111 111 1
 ID 4 CIPSDCPYNNH-COSGK 24

RESULT 2

US-07-609-798-5

Sequence 4, Application US/0993414

Patent No. 5959182

GENERAL INFORMATION:

APPLICANT: ALBERT N. E. SARKIS

APPLICANT: HARMON, HUBERT R.H.

APPLICANT: TYLER, MARCAREL I.

APPLICANT: VANDER, EDWARD J.

TITLE OF INVENTION: Sequenced folding polymers

TITLE OF INVENTION: Folding with (Atax or Hap-lytic) (S) (S)

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Zeno, Inc.

STREET: 1200 South 14th Street

CITY: Richmond

STATE: California

COUNTRY: USA

ZIP: 94804

COMPUTER RELEVABLE FORM:

COMPUTER TYPE: EASY-4.0

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-NT 4.0

SOFTWARE: Patent in Release #1.0, Version #1.2

CURRENT APPLICATION DATA:

FILING DATE: 05/09/99, 41

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

FILING DATE: 17 JULY 1999

APPLICATION NUMBER: 02/007,000

FILING DATE: 27 JULY 1994

APPLICATION NUMBER: 06/015,100

FILING DATE: 29 JAN 1993

APPLICATION NUMBER: 06/007,000

FILING DATE: 31 JAN 1992

PRIORITY APPLICATION:

NAME: Shaw, Melissa A.

REGISTRATION NUMBER: 00,001

REFERENCE NUMBER: 00,001

HYPERTEXT INFORMATION:

TELEPHONE: 510 241 1112

TELEPHONE: 510 241 1112

INFORMATION FOR SEQ ID NO: 41

SEQUENCE CHARACTERISTICS:

LENGTH: 47 amino acids

TYPE: amino acid

FUNCTION: linear

M-LEVEL TYPE: protein

HYPERTEXT: No

ANTI SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Atax robustus
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 47
 OTHER INFORMATION: /label 4
 OTHER INFORMATION: /note "this site may be amplified without loss
 of information of biological activity"
 US 08 943 414 4

Query Match 49.5% Score 709 Lb 17 Length 47
 Best Local Similarity 52.2% Prod. No. 0.054
 Matches 125 Conservative 43 Mismatches 62 Indels 27 Gaps 13

UY 4 CIPSDCPSDHCOSGKAF 26
 1111 1 111 111 1
 ID 4 CIPSDCPYNNH-COSGK 24

RESULT 4

US-07-609-798-5

Sequence 5, Application US/0709098

Patent No. 5241011

GENERAL INFORMATION:

APPLICANT: David Hilliard

APPLICANT: Baldwin, M. Clifford

TITLE OF INVENTION: Sequenced folding polymers

TITLE OF INVENTION: Folding polymers

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Zeno, Inc.

STREET: 1200 South 14th Street

CITY: Richmond

STATE: California

COUNTRY: USA

ZIP: 94804

COMPUTER RELEVABLE FORM:

COMPUTER TYPE: EASY-4.0

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-NT 4.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

FILING DATE: 19/01/98

CLASSIFICATION: 530

PRIORITY APPLICATION DATA:

FILING DATE: 06/01/98

APPLICATION NUMBER: 0000

PRIORITY APPLICATION:

NAME: Westcott, M. Wayne

REGISTRATION NUMBER: 22,700

REFERENCE NUMBER: 00,001

TELEPHONE: (801) 566-6688

TELEPHONE: (801) 566-6688

INFORMATION FOR SEQ ID NO: 5

SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids

TYPE: AMINO ACID

FUNCTION: linear

FUNCTION: peptide

NAME/KEY: 1000 peptide sequence for 1000 loop

IDENTIFICATION WITH THE 1000 peptide sequence for 1000 loop

IDENTIFICATION WITH THE 1000 peptide sequence for 1000 loop

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IDENTIFICATION WITH THE 1000 peptide sequence for 1000 loop

Query Match 37.8% Score 66 DB 1 Length 78
 Best Local Similarity 46.4% Prod. No. 0.29
 Matches 13 Conservative 21 Mismatches 11 Indels 21 Gaps 21

1 2 KWTSBILKERSHIMUSKAT AFW 28
 11 1111 1111 11
 16 51 KWTSBILKERSHIMUSKAT AFW 77

RESULT 4

US-09-749-637a-270-13
 Sequence 13 Application US-09-749-637a-270-13
 Patent No. 5780276

GENERAL INFORMATION:

APPLICANT: Sheng, K1-Joon
 APPLICANT: GILLEY, MARILYN M.
 APPLICANT: GILLEY, MARILYN M.
 TITLE OF INVENTION: COMPOUND FOR PESTICIDE
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Venetian, David J., Howard & Gilletti
 STREET: 1201 New York Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: US
 ZIP: 20005

COMPUTER READABLE FORM:

SEQUENCE TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09-09-749-637a-270-13
 FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/719,554
 FILING DATE: 07-01-1994
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/749,561
 FILING DATE: 17-APR-1995

ATTORNEY/AGENT: INVENTOR:

NAME: Sheng, K1-Joon
 REGISTRATION NUMBER: 28,957

REFERENCE/AGENT NUMBER: 24,60-107674-5
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 962 4813
 TELEFAX: 202 962 8400

INVENTOR: N 18 802 10 N 13
 SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids
 TYPE: amino acid

SEQUENCE: single
 TYPE: linear

MULTIPLE TYPE: protein
 HYDROPHOBIC: N

US-09-749-637a-13

Query Match 37.8% Score 66 DB 1 Length 78
 Best Local Similarity 46.4% Prod. No. 0.29
 Matches 13 Conservative 21 Mismatches 11 Indels 21 Gaps 21

1 2 KWTSBILKERSHIMUSKAT AFW 28
 11 1111 1111 11
 16 51 KWTSBILKERSHIMUSKAT AFW 77

1 2 KWTSBILKERSHIMUSKAT AFW 28
 11 1111 1111 11
 16 51 KWTSBILKERSHIMUSKAT AFW 77

1 2 KWTSBILKERSHIMUSKAT AFW 28
 11 1111 1111 11
 16 51 KWTSBILKERSHIMUSKAT AFW 77

1 2 KWTSBILKERSHIMUSKAT AFW 28
 11 1111 1111 11
 16 51 KWTSBILKERSHIMUSKAT AFW 77

1 2 KWTSBILKERSHIMUSKAT AFW 28
 11 1111 1111 11
 16 51 KWTSBILKERSHIMUSKAT AFW 77

GENERAL INFORMATION:

APPLICANT: Windass, John D.
 TITLE OF INVENTION: Biological Insect Control Agent
 NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZENICA Inc.
 STREET: 1800 Concord Pike

CITY: Wilmington
 STATE: DE

COUNTRY: USA
 ZIP: 19850

COMPUTER READABLE FORM:

SEQUENCE TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09-09-749-637a-270-13
 FILING DATE: 24-SEP-1996
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09-09-749-637a-270-13
 FILING DATE: 27-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09-09-749-637a-270-13
 FILING DATE: 25-MAR-1994
 ATTORNEY/AGENT INFORMATION:

NAME: Holmstedt, Liza D.
 REGISTRATION NUMBER: 27,712

REFERENCE/AGENT NUMBER: 24,60-107674-5
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 866-1694
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE INFORMATION:

LENGTH: 78 amino acids
 TYPE: amino acid

SEQUENCE TYPE: linear

MULTIPLE TYPE: protein

US-09-749-637a-270-13

Query Match 37.8% Score 66 DB 2 Length 78
 Best Local Similarity 46.4% Prod. No. 0.29
 Matches 13 Conservative 21 Mismatches 11 Indels 21 Gaps 21

1 2 KWTSBILKERSHIMUSKAT AFW 28
 11 1111 1111 11
 16 51 KWTSBILKERSHIMUSKAT AFW 77

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1 2 KWTSBILKERSHIMUSKAT AFW 28
 11 1111 1111 11
 16 51 KWTSBILKERSHIMUSKAT AFW 77

CLASSIFICATION: 474
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/06027
 FILING DATE: 27 MAR 1996
 PCT APPLICATION DATA:
 APPLICATION NUMBER: GB 9405951.6
 FILING DATE: 25 MAR 1994
 ALTERNATIVE INVENTION:
 NAME: Baidomero M. Oltorta
 REGISTRATION NUMBER: 44,712
 REFERENCE: 27 MAR 1996
 TELEPHONE: (402) 886-1009
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 Molecule type: Peptide
 US-07-689-637a-6

Query Match: 47.4% Score: 66, 106 Z: Length: 78
 Best Local Similarity: 46.4% Prod. No: 0.29
 Molecule: 12: Conserved: 2: Mismatches: 11: Indels: 2: Gaps: 2:
 11 11 11 11 11 11
 51 FWCWKSCHRMMLDQ NQTAIVLVV 77

RESULT 7
 US-07-689-637a-14
 Sequence: 14: Application PCT/US96/05262
 GENERAL INFORMATION:
 APPLICANT: Shon, Ki Joon
 APPLICANT: Gilley, Michelle M.
 APPLICANT: Oltorta, Baidomero M.
 APPLICANT: Yoshikami, Joji
 APPLICANT: Matsui, Moton
 APPLICANT: Chaz, Louis J.
 APPLICANT: Hilliard, David R.
 TITLE OF INVENTION: Cytotoxic Peptides
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Vardalos, Basil J., Howard & Civillotti, LLP
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER RELEASABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patagon in Release #1.1, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05262
 FILING DATE: 17 APR 1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/422,961
 FILING DATE: 17 APR 1995
 ALTERNATIVE INVENTION:
 NAME: Saxe, Stephen A.
 REGISTRATION NUMBER: 48,609
 REFERENCE: 17 APR 1995
 TELEPHONE: 202-962-9400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids

TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 Molecule type: Peptide
 US-07-689-637a-14

Query Match: 47.4% Score: 66, 106 Z: Length: 78
 Best Local Similarity: 46.4% Prod. No: 0.29
 Molecule: 12: Conserved: 2: Mismatches: 11: Indels: 2: Gaps: 2:
 11 11 11 11 11 11
 51 FWCWKSCHRMMLDQ NQTAIVLVV 77

RESULT 8
 US-07-689-637a-4
 Sequence: 6: Application US/76099-48
 Patent No: 5231011
 GENERAL INFORMATION:
 APPLICANT: David Hilliard
 APPLICANT: Baidomero M. Oltorta
 TITLE OF INVENTION: Sequences of folding determinants
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Theodor, No. 5231011, 5 West 10th
 STREET: 9045 South 700 East, Suite 200
 CITY: Sandy
 STATE: Utah
 COUNTRY: USA
 ZIP: 84070
 COMPUTER RELEASABLE FORM:
 MEDIUM TYPE: diskette, 3.5 inch, 720 Kb storage
 OPERATING SYSTEM: DOS 4.01
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/76099-48
 FILING DATE: 19910418
 CLASSIFICATION: 5:0
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: none
 FILING DATE: na
 ALTERNATIVE INVENTION:
 NAME: Westcott, M. Wayne
 REGISTRATION NUMBER: 22,784
 REFERENCE: 22 MAR 1995
 TELEPHONE: (801) 566-6647
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 Molecule type: peptide
 FEATURE:
 NAME: 6: 27 amino acids
 IDENTIFICATION METHOD: Direct peptide sequencing
 US-07-689-637a-6

Query Match: 47.4% Score: 61, 106 Z: Length: 27
 Best Local Similarity: 44.4% Prod. No: 0.45
 Molecule: 12: Conserved: 2: Mismatches: 11: Indels: 2: Gaps: 2:
 11 11 11 11 11 11
 1 FWCWKSCHRMMLDQ NQTAIVLVV 26

Thu Sep 19 09:49:39 2002

us-09-749-637a-270.ra1

Page 8

Genome version 4.5
Copyright (c) 1993 - 2000 CompuLink Ltd.

Database: Eukaryotic Genomes, Release 2.0 (March 1999)

Run Date: September 19, 2002, 09:19:48 : Search Time: 41.4 Seconds

(without alignments)
121,180 Million cell updates/sec

Filter: 0.5-0.9-749-637a-270

Post-Process: 1.86MTPSDD/PRSDHDP/SGKAPVCL 29

Search: 64,000 seqs, 17,797,929 residues

Total number of hits satisfying chosen parameters: 56,222

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post-Processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database: 1: SP_KEMBL_19:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	Hit	Database
1	72	40.7	78	5	Q90556
2	66	47.3	78	5	Q90555
3	65	46.7	76	5	Q90547
4	64	46.2	75	5	Q90546
5	63.5	45.9	76	5	Q90544
6	63	45.6	76	5	Q90541
7	63.5	44.2	77	5	Q90543
8	63.5	43.6	76	5	Q90545
9	63.5	43.6	77	5	Q90546
10	63.5	43.1	53	12	Q90543
11	63.5	43.1	53	12	Q90543
12	63.5	42.5	71	5	Q90546
13	63.5	42.5	71	5	Q90546
14	63.5	42.5	71	5	Q90546
15	63.5	42.5	71	5	Q90546
16	63.5	42.5	71	5	Q90546

Result No.	Score	Match	Length	Hit	Database
17	63.5	42.5	71	5	Q90546
18	63.5	42.5	71	5	Q90546
19	63.5	42.5	71	5	Q90546
20	63.5	42.5	71	5	Q90546
21	63.5	42.5	71	5	Q90546
22	63.5	42.5	71	5	Q90546
23	63.5	42.5	71	5	Q90546
24	63.5	42.5	71	5	Q90546
25	63.5	42.5	71	5	Q90546
26	63.5	42.5	71	5	Q90546
27	63.5	42.5	71	5	Q90546
28	63.5	42.5	71	5	Q90546
29	63.5	42.5	71	5	Q90546
30	63.5	42.5	71	5	Q90546
31	63.5	42.5	71	5	Q90546
32	63.5	42.5	71	5	Q90546
33	63.5	42.5	71	5	Q90546
34	63.5	42.5	71	5	Q90546
35	63.5	42.5	71	5	Q90546
36	63.5	42.5	71	5	Q90546
37	63.5	42.5	71	5	Q90546
38	63.5	42.5	71	5	Q90546
39	63.5	42.5	71	5	Q90546
40	63.5	42.5	71	5	Q90546
41	63.5	42.5	71	5	Q90546
42	63.5	42.5	71	5	Q90546
43	63.5	42.5	71	5	Q90546
44	63.5	42.5	71	5	Q90546
45	63.5	42.5	71	5	Q90546

ALIGNMENTS

RESULT 1

Q90556 1: SP_KEMBL_19:*

Q90556 2: SP_KEMBL_19:*

Q90556 3: SP_KEMBL_19:*

Q90556 4: SP_KEMBL_19:*

Q90556 5: SP_KEMBL_19:*

Q90556 6: SP_KEMBL_19:*

Q90556 7: SP_KEMBL_19:*

Q90556 8: SP_KEMBL_19:*

Q90556 9: SP_KEMBL_19:*

Q90556 10: SP_KEMBL_19:*

Q90556 11: SP_KEMBL_19:*

Q90556 12: SP_KEMBL_19:*

Q90556 13: SP_KEMBL_19:*

Q90556 14: SP_KEMBL_19:*

Q90556 15: SP_KEMBL_19:*

Q90556 16: SP_KEMBL_19:*

Q90556 17: SP_KEMBL_19:*

Q90556 18: SP_KEMBL_19:*

Q90556 19: SP_KEMBL_19:*

Q90556 20: SP_KEMBL_19:*

Q90556 21: SP_KEMBL_19:*

Q90556 22: SP_KEMBL_19:*

Q90556 23: SP_KEMBL_19:*

Q90556 24: SP_KEMBL_19:*

Q90556 25: SP_KEMBL_19:*

Q90556 26: SP_KEMBL_19:*

Q90556 27: SP_KEMBL_19:*

Q90556 28: SP_KEMBL_19:*

Q90556 29: SP_KEMBL_19:*

Q90556 30: SP_KEMBL_19:*

Q90556 31: SP_KEMBL_19:*

Q90556 32: SP_KEMBL_19:*

Q90556 33: SP_KEMBL_19:*

Q90556 34: SP_KEMBL_19:*

Q90556 35: SP_KEMBL_19:*

Q90556 36: SP_KEMBL_19:*

Q90556 37: SP_KEMBL_19:*

Q90556 38: SP_KEMBL_19:*

Q90556 39: SP_KEMBL_19:*

Q90556 40: SP_KEMBL_19:*

Q90556 41: SP_KEMBL_19:*

Q90556 42: SP_KEMBL_19:*

Q90556 43: SP_KEMBL_19:*

Q90556 44: SP_KEMBL_19:*

Q90556 45: SP_KEMBL_19:*

GeneBank version 4.5
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EM protein - protein search using sw model

September 19, 2002, 09:29:22 : Search time 11.19 seconds
(without alignment)
85130 Million cell updates/sec

Title: us-09-749-637a-270
Percent score: 177
Sequence: 1 LRWCPSPDQCFRSHDIGNSKAFVCL 29

Scoring tables: BLOSUM62
Gapop 10.0, Gapext 0.5

Source(s): 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum hit seq length: 0
Maximum hit seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: 1 SwissProt_40.*

Print: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	Description
1	66	47.3	27	1	EXHA_CONTE	EXHA_CONTE
2	66	47.3	27	1	EXHA_CONTE	EXHA_CONTE
3	65	46.2	26	1	EXHA_CONTE	EXHA_CONTE
4	64	36.2	27	1	EXHA_CONTE	EXHA_CONTE
5	60	33.9	26	1	EXHA_CONTE	EXHA_CONTE
6	60	33.9	26	1	EXHA_CONTE	EXHA_CONTE
7	58.5	33.1	27	1	EXHA_CONTE	EXHA_CONTE
8	58	32.8	27	1	EXHA_CONTE	EXHA_CONTE
9	58	32.8	27	1	EXHA_CONTE	EXHA_CONTE
10	57.5	31.9	27	1	EXHA_CONTE	EXHA_CONTE
11	56.5	31.9	27	1	EXHA_CONTE	EXHA_CONTE
12	56.5	31.9	27	1	EXHA_CONTE	EXHA_CONTE
13	56	31.6	27	1	EXHA_CONTE	EXHA_CONTE
14	56	31.6	27	1	EXHA_CONTE	EXHA_CONTE
15	55	31.1	27	1	EXHA_CONTE	EXHA_CONTE
16	55	31.1	27	1	EXHA_CONTE	EXHA_CONTE
17	55	31.1	27	1	EXHA_CONTE	EXHA_CONTE
18	55	31.1	27	1	EXHA_CONTE	EXHA_CONTE
19	54.5	30.8	27	1	EXHA_CONTE	EXHA_CONTE
20	54	30.5	27	1	EXHA_CONTE	EXHA_CONTE
21	54	30.5	27	1	EXHA_CONTE	EXHA_CONTE
22	54	30.5	27	1	EXHA_CONTE	EXHA_CONTE
23	54	30.5	27	1	EXHA_CONTE	EXHA_CONTE
24	53	29.9	27	1	EXHA_CONTE	EXHA_CONTE
25	52	29.4	27	1	EXHA_CONTE	EXHA_CONTE
26	51.5	29.1	27	1	EXHA_CONTE	EXHA_CONTE
27	51	28.8	27	1	EXHA_CONTE	EXHA_CONTE
28	50	28.2	27	1	EXHA_CONTE	EXHA_CONTE
29	50	28.2	27	1	EXHA_CONTE	EXHA_CONTE
30	49.5	28.3	27	1	EXHA_CONTE	EXHA_CONTE
31	49.5	28.3	27	1	EXHA_CONTE	EXHA_CONTE
32	49	27.7	24	1	EXHA_CONTE	EXHA_CONTE
33	49	27.7	24	1	EXHA_CONTE	EXHA_CONTE

ALIGNMENTS

Result	Score	Query	Match	Length	DB	Description
1	66	47.3	27	1	EXHA_CONTE	EXHA_CONTE
2	66	47.3	27	1	EXHA_CONTE	EXHA_CONTE
3	65	46.2	26	1	EXHA_CONTE	EXHA_CONTE
4	64	36.2	27	1	EXHA_CONTE	EXHA_CONTE
5	60	33.9	26	1	EXHA_CONTE	EXHA_CONTE
6	60	33.9	26	1	EXHA_CONTE	EXHA_CONTE
7	58.5	33.1	27	1	EXHA_CONTE	EXHA_CONTE
8	58	32.8	27	1	EXHA_CONTE	EXHA_CONTE
9	58	32.8	27	1	EXHA_CONTE	EXHA_CONTE
10	57.5	31.9	27	1	EXHA_CONTE	EXHA_CONTE
11	56.5	31.9	27	1	EXHA_CONTE	EXHA_CONTE
12	56.5	31.9	27	1	EXHA_CONTE	EXHA_CONTE
13	56	31.6	27	1	EXHA_CONTE	EXHA_CONTE
14	56	31.6	27	1	EXHA_CONTE	EXHA_CONTE
15	55	31.1	27	1	EXHA_CONTE	EXHA_CONTE
16	55	31.1	27	1	EXHA_CONTE	EXHA_CONTE
17	55	31.1	27	1	EXHA_CONTE	EXHA_CONTE
18	55	31.1	27	1	EXHA_CONTE	EXHA_CONTE
19	54.5	30.8	27	1	EXHA_CONTE	EXHA_CONTE
20	54	30.5	27	1	EXHA_CONTE	EXHA_CONTE
21	54	30.5	27	1	EXHA_CONTE	EXHA_CONTE
22	54	30.5	27	1	EXHA_CONTE	EXHA_CONTE
23	54	30.5	27	1	EXHA_CONTE	EXHA_CONTE
24	53	29.9	27	1	EXHA_CONTE	EXHA_CONTE
25	52	29.4	27	1	EXHA_CONTE	EXHA_CONTE
26	51.5	29.1	27	1	EXHA_CONTE	EXHA_CONTE
27	51	28.8	27	1	EXHA_CONTE	EXHA_CONTE
28	50	28.2	27	1	EXHA_CONTE	EXHA_CONTE
29	50	28.2	27	1	EXHA_CONTE	EXHA_CONTE
30	49.5	28.3	27	1	EXHA_CONTE	EXHA_CONTE
31	49.5	28.3	27	1	EXHA_CONTE	EXHA_CONTE
32	49	27.7	24	1	EXHA_CONTE	EXHA_CONTE
33	49	27.7	24	1	EXHA_CONTE	EXHA_CONTE

[illegible]

PI VARIANT 195 195 M V.
 SEQ ENTRE 197 AA: 21248 MW: 199088489674579 CR664:

Query Match 31.6% Score 56; DH 1; Length 197;
 Host Local Similarity 44.0% Pred. No. 1.9;
 Mismatches 11; Conservative 4; Mismatches 19; Indels 2; Gaps 1;

Q 4 CIPSDGCTPSDHIQVSGKAEV 28
 I 1 1 1 1 1 1 1
 I 0 79 CKNSEHIT--DHAGTKKPIV 101

RESULT 15

TX BLATVE STANDARD; PRT; 37 AA.

15-JUL-1999 (rel. 38; Created)

15-JUL-1999 (rel. 38; last sequence update)

01-MAR-2002 (rel. 41; last annotation update)

FE omega-aristoloxin Hv1b (omega-ArTX-Hv1b);

OS Hadronyche versata (Blue mountain funnel web spider) (Arax

OS versatus);

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;

OC Mesothelphae; Hexathe-lidae; Hadronychae;

OX NCBI_TaxID:6504;

KN 11;

KP SPIDRNC;

KC TISSUE-Venom;

KX MEDLINE:99421654; PubMed:10491055;

KA Wain X.-H., Smith R., Fletcher J.L., Wilson H., Wood G.J.,

RA Morlin E.H., King G.F.;

RT "Structure-function studies of omega-aristoloxin, a potent antagonist

RT of insect voltage-gated calcium channels.";

RL Eur. J. Biochem. 264:488-494(1999)

OC 1- FUNCTION: INHIBITS INSECT, BUT NOT MAMMALIAN, VOLTAGE-GATED

OC CALCIUM CHANNEL CURRENTS.

OC 1- SUBCELLULAR LOCATION: Secreted.

OC HEST: J56207; IAXH.

KW calcium channel inhibitor; toxin; Neurotoxin.

E1 HISGEPD 4 18 BY SIMILARITY.

E1 DLSGEPD 11 22 BY SIMILARITY.

E1 DLSGEPD 17 26 BY SIMILARITY.

SEQUENCE 37 AA: 4061 MW: A115058959014EZF CR664;

Query Match 41.1% Score 55; DH 1; Length 37;
 Host Local Similarity 43.7% Pred. No. 0.7;
 Mismatches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

Q 4 CIPSDGCTPSDHIQVSGKAE 26
 I 1 1 1 1 1 1 1
 I 0 4 CIPSDGCTPSDHIQVSGKAE 24

Search completed: September 19, 2002, 09:27:03

Job time: 400 sec



A.Molecule type: mRNA
 Accession: U54 - EHD
 Accession references: chr1:2858, chr1:450706, chr1:450706, chr1:450706, chr1:450706
 Accession: A018X

Query Match 40.5% Score 54.5 Length 54
 Best Local Similarity 47.9% Prod. No. 4.67
 Matches 11: Conservative 5: Mismatches 8: Indels 5: Gaps 2:

QY 4 CTPSDH/FRSHD/CSKAVV-----CSKAVV 28
 1 1 1 1 1 1 1 1 1 1 1 1
 LE 25 CAVTAVVWVNE--CSKAVVSVNVT 51

RESULT 12
 S47577
 Metallothionein 20-111B - Blue mussel
 C.Specific: Mytilus edulis (blue mussel)
 C.Date: 27 Jan 1995 #sequence revision 18 Jan 1995 #ext_change 17 Mar 1999
 C.Accession: S47577

R.Mackay, E.A. Overholt, J. Pankat, R. Lewis, L. Brinkley, P. J. Kasin, J.H.R. F
 Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
 A.Accession: S47577
 A.Reference number: S39416; M01D:94062828

A.Molecule type: Protein
 C.Specific: metallothionein
 C.Keywords: chelation; metal binding

Query Match 40.5% Score 54.5 Length 71
 Best Local Similarity 46.4% Prod. No. 6.52
 Matches 12: Conservative 1: Mismatches 12: Indels 0: Gaps 1:

QY 4 CTPSDH/FRSHD/CSKAVV-----CSKAVV 28
 1 1 1 1 1 1 1 1 1 1 1 1
 LE 22 CCGDHWKVASGSCSKKVVWVSSIVNVP 54

RESULT 13
 S39422
 Metallothionein 20-111A - Blue mussel
 C.Specific: Mytilus edulis (blue mussel)
 C.Date: 14 Jan 1995 #sequence revision 18 Jan 1995 #ext_change 17 Mar 1999
 C.Accession: S39422

R.Mackay, E.A. Overholt, J. Pankat, R. Lewis, L. Brinkley, P. J. Kasin, J.H.R. F
 Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
 A.Accession: S39422
 A.Reference number: M01D:94062828

A.Molecule type: Protein
 C.Specific: metallothionein
 C.Keywords: chelation; metal binding

C.Date: 20 Aug 1999 #sequence revision 20 Aug 1999 #ext_change 24 May 2001
 C.Accession: D44007

R.Skinner, W.S. Jennings, P.A. Li, J.P. Gustad, G.H.
 Toxinom 30, 1043-1050 1992
 A.Title: Identification of insecticidal peptides from venom of the trap-door spider
 A.Reference number: A44007; M01D:94062979
 A.Accession: D44007

A.Molecule type: Protein
 A.Residues: 1-76 - SKT
 A.Cross reference: P108:AAH24049.1; P108:459240
 A.Note: sequence extracted from NBI database (NBI:P-119527)
 C.Keywords: disulfide bond; toxin; venom

Query Match 40.5% Score 54.5 Length 76
 Best Local Similarity 45.5% Prod. No. 6.37
 Matches 10: Conservative 1: Mismatches 9: Indels 2: Gaps 1:

QY 2 RWC2PSM42FRSHD/SSSKK 23
 1 1 1 1 1 1 1 1 1 1
 LE 21 CWTGDSVSSSSS--SSSKK 40

RESULT 15
 C44007
 Atoxin VI - trap-door spider (Apostichus schlingerii)
 N.Alternate names: insecticidal peptide Aps VI
 C.Specific: Apostichus schlingerii
 C.Date: 20 Aug 1999 #sequence revision 20 Aug 1999 #ext_change 24 May 2001
 C.Accession: C44007

R.Skinner, W.S. Jennings, P.A. Li, J.P. Gustad, G.H.
 Toxinom 30, 1043-1050 1992
 A.Title: Identification of insecticidal peptides from venom of the trap-door spider
 A.Reference number: A44007; M01D:94062979
 A.Accession: C44007

A.Molecule type: Protein
 A.Residues: 1-76 - SKT
 A.Cross reference: P108:AAH24049.1; P108:459240
 A.Note: sequence extracted from NBI database (NBI:P-119529)
 C.Keywords: disulfide bond; toxin; venom

Query Match 40.5% Score 54.5 Length 76
 Best Local Similarity 45.5% Prod. No. 6.37
 Matches 10: Conservative 1: Mismatches 9: Indels 2: Gaps 1:

QY 2 RWC2PSM42FRSHD/SSSKK 23
 1 1 1 1 1 1 1 1 1 1
 LE 21 CWTGDSVSSSSS--SSSKK 40

RESULT 16
 S44007
 Atoxin VI - trap-door spider (Apostichus schlingerii)
 N.Alternate names: insecticidal peptide Aps VI
 C.Specific: Apostichus schlingerii

